

=> d his

(FILE 'HOME' ENTERED AT 15:05:47 ON 15 AUG 2006)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 15:06:00 ON 15 AUG 2006

L1	0 S LT-B-R
L2	637 S LYMPHOTOXIN (3W) BETA (W) RECEPTOR
L3	62 S L2 (S) FUSION
L4	17 S L3 (S) (ADMINISTRATION OR ADMINISTER OR ADMINISTERS OR TREAT
L5	8 DUP REM L4 (9 DUPLICATES REMOVED)
L6	0 S L3 (P) OPHTHALMIA
L7	0 S L2 (P) OPHTHALMIA
L8	0 S L2 (P) OPHTHALMIA
L9	1069 S LYMPHOTOXIN (W) BETA
L10	0 S L9 (P) OPHTHALMIA
L11	0 S SYMPHATHETIC (W) OPHTHALMIA
L12	30 S OPHTHALMIA
L13	30 DUP REM L12 (0 DUPLICATES REMOVED)
L14	0 S L13 (S) (AUTOIMMUNE OR TH)
L15	1131 S SYMPATHETIC (W) OPHTHALMIA
L16	0 S L15 (S) (AUTOIMMUE OR TH)
L17	39 S L15 (S) AUTOIMMUNE
L18	23 DUP REM L17 (16 DUPLICATES REMOVED)
L19	0 S L15 (S) (TH (W) CELL)

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1051	Browning.IN.	US-PGPUB; USPAT	OR	ON	2006/08/15 13:52
L2	31	L1 and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:35
L3	28	Benjamin.IN. and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:30
L4	5	Hochman.IN. and lymphotoxin	US-PGPUB; USPAT	OR	ON	2006/08/15 14:35

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.ra1.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:31:35 ; Search time 49 Seconds  
(without alignments)  
351.909 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1133	100.0	197	1	US-08-505-606-1 Sequence 1, Appli
2	1133	100.0	197	2	US-09-000-166-1 Sequence 1, Appli
3	1133	100.0	197	2	US-09-303-262-1 Sequence 1, Appli
4	1133	100.0	473	2	US-09-949-016-7944 Sequence 7944, Ap
5	987	87.1	170	2	US-08-828-683A-14 Sequence 14, Appl
6	981	86.6	170	2	US-09-523-323-57 Sequence 57, Appl
7	771	68.0	415	2	US-09-006-353A-6 Sequence 6, Appli
8	771	68.0	415	2	US-09-573-986-6 Sequence 6, Appli
9	456	40.2	77	2	US-08-866-545-3 Sequence 3, Appli

10	456	40.2	77	2	US-09-627-775-3	Sequence 3, Appli
11	305	26.9	227	2	US-08-974-022-48	Sequence 48, Appl
12	305	26.9	227	2	US-08-795-445A-48	Sequence 48, Appl
13	305	26.9	227	2	US-08-795-447A-48	Sequence 48, Appl
14	305	26.9	227	2	US-08-974-186-48	Sequence 48, Appl
15	305	26.9	227	2	US-08-795-446B-48	Sequence 48, Appl
16	305	26.9	227	2	US-08-706-945D-134	Sequence 134, App
17	305	26.9	227	2	US-08-577-788C-48	Sequence 48, Appl
18	305	26.9	235	2	US-09-326-394-4	Sequence 4, Appli
19	305	26.9	235	2	US-09-580-235-2	Sequence 2, Appli
20	305	26.9	235	2	US-09-580-235-8	Sequence 8, Appli
21	305	26.9	235	2	US-09-580-181-2	Sequence 2, Appli
22	305	26.9	235	2	US-09-580-181-8	Sequence 8, Appli
23	305	26.9	235	2	US-09-102-530-2	Sequence 2, Appli
24	305	26.9	235	2	US-09-102-530-8	Sequence 8, Appli
25	305	26.9	235	2	US-09-882-735A-16	Sequence 16, Appl
26	305	26.9	257	2	US-09-579-845-10	Sequence 10, Appl
27	305	26.9	439	2	US-10-360-101-226	Sequence 226, App
28	305	26.9	461	1	US-08-385-229-2	Sequence 2, Appli
29	305	26.9	461	1	US-08-650-000-2	Sequence 2, Appli
30	305	26.9	461	2	US-09-042-785A-7	Sequence 7, Appli
31	305	26.9	461	2	US-08-477-347-3	Sequence 3, Appli
32	305	26.9	461	2	US-09-006-353A-4	Sequence 4, Appli
33	305	26.9	461	2	US-08-476-862-2	Sequence 2, Appli
34	305	26.9	461	2	US-09-573-986-4	Sequence 4, Appli
35	305	26.9	461	2	US-08-406-824A-2	Sequence 2, Appli
36	305	26.9	461	2	US-09-800-909-2	Sequence 2, Appli
37	305	26.9	461	2	US-09-758-124-2	Sequence 2, Appli
38	305	26.9	461	2	US-09-800-908-3	Sequence 3, Appli
39	305	26.9	461	2	US-09-896-096A-17	Sequence 17, Appl
40	305	26.9	461	2	US-09-949-016-6019	Sequence 6019, Ap
41	305	26.9	461	2	US-10-046-433-6	Sequence 6, Appli
42	305	26.9	461	7	5395760-2	Patent No. 5395760
43	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
44	305	26.9	491	2	US-09-949-016-7840	Sequence 7840, Ap
45	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rapbm.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:43:31 ; Search time 176 Seconds  
(without alignments)  
518.485 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1133	100.0	197	4	US-10-003-211-1
2	1133	100.0	197	5	US-10-077-406-1
3	1133	100.0	435	3	US-09-907-372-19
4	1133	100.0	435	3	US-09-768-779A-6
5	1133	100.0	435	3	US-09-917-372-19
6	1133	100.0	435	4	US-10-087-192-942
7	1133	100.0	435	4	US-10-291-480-6
8	1133	100.0	435	4	US-10-369-300-17
9	1133	100.0	435	4	US-10-262-445-133
10	1133	100.0	435	6	US-11-077-386-19

11	1133	100.0	450	6	US-11-077-386-20	Sequence 20, Appl
12	1129	99.6	399	3	US-09-907-372-1	Sequence 1, Appli
13	1129	99.6	399	3	US-09-917-372-1	Sequence 1, Appli
14	1129	99.6	399	6	US-11-077-386-18	Sequence 18, Appl
15	1108	97.8	416	5	US-10-484-148-16	Sequence 16, Appl
16	987	87.1	170	4	US-10-112-793-14	Sequence 14, Appl
17	970	85.6	172	4	US-10-375-680-57	Sequence 57, Appl
18	780	68.8	257	3	US-09-948-018-19	Sequence 19, Appl
19	771	68.0	402	4	US-10-087-192-939	Sequence 939, App
20	771	68.0	415	3	US-09-826-212-6	Sequence 6, Appli
21	771	68.0	415	3	US-09-907-372-20	Sequence 20, Appl
22	771	68.0	415	3	US-09-935-727-8	Sequence 8, Appli
23	771	68.0	415	3	US-09-917-372-20	Sequence 20, Appl
24	771	68.0	415	4	US-10-186-643-6	Sequence 6, Appli
25	771	68.0	415	4	US-10-418-242-8	Sequence 8, Appli
26	771	68.0	415	5	US-10-943-197-47	Sequence 47, Appl
27	771	68.0	415	6	US-11-182-946-6	Sequence 6, Appli
28	381.5	33.7	305	4	US-10-264-049-3058	Sequence 3058, Ap
29	311.5	27.5	659	4	US-10-363-427-12	Sequence 12, Appl
30	307	27.1	720	4	US-10-363-427-8	Sequence 8, Appli
31	305	26.9	225	3	US-09-840-795-10	Sequence 10, Appl
32	305	26.9	227	3	US-09-405-032-131	Sequence 131, App
33	305	26.9	227	5	US-10-762-159-131	Sequence 131, App
34	305	26.9	235	3	US-09-102-530-2	Sequence 2, Appli
35	305	26.9	235	3	US-09-102-530-8	Sequence 8, Appli
36	305	26.9	235	3	US-09-907-263-4	Sequence 4, Appli
37	305	26.9	235	3	US-09-882-735-16	Sequence 16, Appl
38	305	26.9	235	4	US-10-243-230-2	Sequence 2, Appli
39	305	26.9	235	4	US-10-243-230-8	Sequence 8, Appli
40	305	26.9	235	4	US-10-436-826-75	Sequence 75, Appl
41	305	26.9	235	4	US-10-621-783-4	Sequence 4, Appli
42	305	26.9	235	4	US-10-622-383-4	Sequence 4, Appli
43	305	26.9	235	6	US-11-126-126-16	Sequence 16, Appl
44	305	26.9	257	4	US-10-313-852-10	Sequence 10, Appl
45	305	26.9	257	4	US-10-314-033-10	Sequence 10, Appl

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:44:06 ; Search time 31 Seconds  
(without alignments)  
419.700 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1133	100.0	197	6	US-10-533-153-1 Sequence 1, Appli
2	305	26.9	355	6	US-10-504-973-33 Sequence 33, Appl
3	305	26.9	461	6	US-10-511-937-2945 Sequence 2945, Ap
4	305	26.9	461	7	US-11-183-218-32 Sequence 32, Appl
5	295.5	26.1	278	7	US-11-170-797-16 Sequence 16, Appl
6	290	25.6	258	6	US-10-643-589-4 Sequence 4, Appli
7	280	24.7	237	6	US-10-504-973-22 Sequence 22, Appl
8	278	24.5	197	7	US-11-211-917-139 Sequence 139, App

9	278	24.5	277	6	US-10-511-937-2518	Sequence 2518, Ap
10	278	24.5	277	7	US-11-170-797-5	Sequence 5, Appli
11	251.5	22.2	269	7	US-11-170-797-19	Sequence 19, Appl
12	243.5	21.5	289	7	US-11-170-797-12	Sequence 12, Appl
13	239.5	21.1	349	7	US-11-175-714-67	Sequence 67, Appl
14	239.5	21.1	401	7	US-11-175-714-54	Sequence 54, Appl
15	230.5	20.3	283	6	US-10-539-228-546	Sequence 546, App
16	230.5	20.3	283	6	US-10-539-228-548	Sequence 548, App
17	230.5	20.3	283	6	US-10-539-228-550	Sequence 550, App
18	228.5	20.2	655	6	US-10-505-928-843	Sequence 843, App
19	228.5	20.2	655	6	US-10-196-749-418	Sequence 418, App
20	205	18.1	247	6	US-10-504-973-6	Sequence 6, Appli
21	201	17.7	277	6	US-10-511-937-2455	Sequence 2455, Ap
22	198	17.5	153	7	US-11-211-917-140	Sequence 140, App
23	195.5	17.3	255	6	US-10-623-808-8	Sequence 8, Appli
24	195.5	17.3	255	6	US-10-539-257-2	Sequence 2, Appli
25	195.5	17.3	255	7	US-11-128-422-8	Sequence 8, Appli
26	182	16.1	194	6	US-10-539-228-543	Sequence 543, App
27	179.5	15.8	256	6	US-10-623-808-6	Sequence 6, Appli
28	179.5	15.8	256	7	US-11-128-422-6	Sequence 6, Appli
29	172.5	15.2	250	7	US-11-320-192-11	Sequence 11, Appl
30	171.5	15.1	251	7	US-11-320-192-8	Sequence 8, Appli
31	167.5	14.8	440	7	US-11-254-182-49	Sequence 49, Appl
32	156	13.8	411	7	US-11-254-182-47	Sequence 47, Appl
33	156	13.8	411	7	US-11-297-319-1	Sequence 1, Appli
34	152.5	13.5	243	7	US-11-320-192-9	Sequence 9, Appli
35	152.5	13.5	243	7	US-11-320-192-12	Sequence 12, Appl
36	150.5	13.3	250	7	US-11-320-192-10	Sequence 10, Appl
37	148.5	13.1	250	7	US-11-320-192-7	Sequence 7, Appli
38	146.5	12.9	111	7	US-11-211-917-141	Sequence 141, App
39	145	12.8	60	6	US-10-560-025-37	Sequence 37, Appl
40	140.5	12.4	417	6	US-10-505-928-793	Sequence 793, App
41	137.5	12.1	468	6	US-10-511-937-2595	Sequence 2595, Ap
42	133.5	11.8	417	6	US-10-196-749-474	Sequence 474, App
43	132.5	11.7	575	7	US-11-217-997-32	Sequence 32, Appl
44	132.5	11.7	1547	7	US-11-217-997-22	Sequence 22, Appl
45	132.5	11.7	1577	7	US-11-217-997-16	Sequence 16, Appl



This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rpr.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:26:35 ; Search time 41 Seconds  
(without alignments)  
462.310 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1133	100.0	435	2	I54182	tumor necrosis fac
2	305	26.9	461	1	A35356	tumor necrosis fac
3	295	26.0	474	2	B38634	tumor necrosis fac
4	290	25.6	459	2	I48854	gene murine tumour
5	278	24.5	277	2	A60771	B-cell activation
6	243.5	21.5	305	2	A46476	B cell-associated
7	226.5	20.0	651	2	JC7705	death receptor-6 -
8	222.5	19.6	271	2	S12783	OX40 antigen precu
9	214.5	18.9	272	2	I48700	gene ox40 protein
10	210.5	18.6	455	1	GQHUT1	tumor necrosis fac
11	210	18.5	348	2	T28623	hypothetical prote
12	210	18.5	349	2	D36858	gene G4R protein -

13	207	18.3	349	2	D72175	G2R protein - vari
14	206	18.2	461	2	JC4302	tumor necrosis fac
15	201	17.7	277	2	I37552	OX40 homolog - hum
16	201	17.7	454	1	GQMST1	tumor necrosis fac
17	196	17.3	595	2	A42086	CD30 antigen precu
18	195.5	17.3	255	2	I38426	lymphocyte activat
19	189	16.7	325	2	B43692	T2 protein - rabbi
20	187.5	16.5	314	2	I37383	FAS soluble protei
21	184.5	16.3	461	1	GQRTT1	tumor necrosis fac
22	183.5	16.2	326	1	GQVZML	T2 protein - myxom
23	181	16.0	335	2	A40036	apoptosis-mediatin
24	179.5	15.8	256	2	B32393	T-cell antigen 4-1
25	171.5	15.1	425	1	A26431	nerve growth facto
26	166	14.7	493	2	JC5486	membrane glycoprot
27	164	14.5	416	1	JN0006	nerve growth facto
28	162	14.3	327	2	A46484	apoptosis-mediatin
29	148.5	13.1	427	1	GQHUN	nerve growth facto
30	145.5	12.8	324	2	JC2395	Fas antigen precur
31	133	11.7	260	1	A46517	CD27 antigen precu
32	132.5	11.7	1111	2	T26972	hypothetical prote
33	129.5	11.4	1620	2	T27283	hypothetical prote
34	129	11.4	3084	1	MMMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2	T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2	T42017	cysteine rich prot
37	126	11.1	3635	2	T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2	T29764	hypothetical prote
39	124.5	11.0	899	2	G02428	subtilisin-like pr
40	124.5	11.0	915	2	JC6148	subtilisin-like pr
41	124.5	11.0	3707	2	S18252	heparan sulfate pr
42	124	10.9	1680	2	A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2	JC7569	Delta-4 protein -
44	123	10.9	722	2	I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1	A48225	subtilisin-like pr

This page gives you Search Results detail for the Application 10077406 and Search Result us-10-077-406-1.rup.

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OM protein - protein search, using sw model

Run on: July 31, 2006, 19:23:10 ; Search time 300 Seconds  
(without alignments)  
607.427 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQPQAVPPYASENQTCRDQE.....QSDTTCKNPLEPLPPEMSGT 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1133	100.0	435	1	TNR3_HUMAN	P36941 homo sapien
2	1098	96.9	435	2	Q5RDW2_PONPY	Q5rdw2 pongo pygma
3	771	68.0	415	1	TNR3_MOUSE	P50284 mus musculu
4	771	68.0	415	2	Q3UK82_MOUSE	Q3uk82 mus musculu
5	749.5	66.2	416	2	Q5U2S8_RAT	Q5u2s8 rattus norv
6	323	28.5	459	2	Q3MHI9_BOVIN	Q3mhi9 bos taurus
7	309.5	27.3	483	2	Q800K7_PAROL	Q800k7 paralichthy
8	305	26.9	461	1	TNR1B_HUMAN	P20333 h tumor nec
9	305	26.9	461	2	Q5THJ6_HUMAN	Q5thj6 homo sapien
10	298.5	26.3	313	2	Q4G265_HORSE	Q4g265 equus cabal
11	295.5	26.1	278	2	Q8SQ34_PIG	Q8sq34 sus scrofa
12	295	26.0	474	1	TNR1B_MOUSE	P25119 mus musculu
13	295	26.0	474	2	Q545P4_MOUSE	Q545p4 m adult mal
14	291.5	25.7	433	2	Q91ZM6_RAT	Q91zm6 rattus norv

15	291.5	25.7	461	2	Q6VAU8_RAT	Q6vau8	rattus norv
16	291.5	25.7	474	1	TNR1B_RAT	Q80wy6	rattus norv
17	291.5	25.7	474	2	Q5YLP0_RAT	Q5ylp0	rattus norv
18	290	25.6	459	2	Q62327_MOUSE	Q62327	mus musculu
19	290	25.6	474	2	Q3U2A9_MOUSE	Q3u2a9	mus musculu
20	285.5	25.2	300	1	TNR6B_HUMAN	O95407	homo sapien
21	284.5	25.1	274	1	TNR5_CANFA	Q7yrl5	canis famil
22	283	25.0	625	1	TNR11_MOUSE	O35305	mus musculu
23	282	24.9	277	2	Q53GN5_HUMAN	Q53gn5	homo sapien
24	280	24.7	274	2	Q3LRP1_CALJA	Q3lrp1	callithrix
25	278	24.5	223	2	Q86YK5_HUMAN	Q86yk5	homo sapien
26	278	24.5	277	1	TNR5_HUMAN	P25942	homo sapien
27	278	24.5	277	2	Q5U007_HUMAN	Q5u007	homo sapien
28	277	24.4	321	2	Q59EP9_HUMAN	Q59ep9	homo sapien
29	277	24.4	616	1	TNR11_HUMAN	Q9y6q6	homo sapien
30	276	24.4	302	2	Q4SNE8_TETNG	Q4sne8	tetraodon n
31	273.5	24.1	280	2	Q3ZTK5_HORSE	Q3ztk5	equus cabal
32	266.5	23.5	387	2	Q6GLN3_XENLA	Q6gln3	xenopus lae
33	265.5	23.4	277	2	Q8WMQ2_SHEEP	Q8wmq2	ovis aries
34	265	23.4	289	2	Q4QQW2_RAT	Q4qqw2	rattus norv
35	258	22.8	275	2	Q3SXX1_MOUSE	Q3sxx1	mus musculu
36	258	22.8	275	2	Q80WM9_MOUSE	Q80wm9	mus musculu
37	258	22.8	276	2	Q71F55_MOUSE	Q71f55	mus musculu
38	253	22.3	462	2	Q5ZL08_CHICK	Q5zl08	gallus gall
39	253	22.3	462	2	Q805B0_CHICK	Q805b0	gallus gall
40	252.5	22.3	203	2	Q5JY15_HUMAN	Q5jy15	homo sapien
41	252.5	22.3	402	2	Q4F9K2_CHICK	Q4f9k2	gallus gall
42	251.5	22.2	269	1	TNR5_BOVIN	Q28203	bos taurus
43	246.5	21.8	401	2	Q6PI12_MOUSE	Q6pi12	mus musculu
44	245	21.6	278	2	Q5BK53_RAT	Q5bk53	rattus norv
45	243.5	21.5	289	1	TNR5_MOUSE	P27512	mus musculu